SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Horvitz, Robert
            Yuan, Junying
            Shaham, Shai

(ii) TITLE OF THE INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
        BETA CONVERTASE GENE TO A C. ELEGANS CELL DEATH
        GENE, INHIBITORY PORTIONS OF THESE GENES AND...

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Clark & Elbing LLP
    (B) STREET: 176 Federal Street
    (C) CITY: Boston
    (D) STATE: MA
    (E) COUNTRY: USA
    (F) ZIP: 02110

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette
    (B) COMPUTER: IBM Compatible
    (C) OPERATING SYSTEM: DOS
    (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE: 21-MAY-1995
    (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/394,189
    (B) FILING DATE: 24-FEB-1995

    (A) APPLICATION NUMBER: 08/282,211
    (B) FILING DATE: 12-JUL-1994

    (A) APPLICATION NUMBER: 07/984,182
    (B) FILING DATE: 20-NOV-1992

    (A) APPLICATION NUMBER: 07/897,788
    (B) FILING DATE: 12-JUN-1992

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Bieker-Brady, Kristina
    (B) REGISTRATION NUMBER: 39,109

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 7653 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTGTCGAATT AATATCCCTA TTATCACTTT TTCATGCTCA TCCTCGAGCG GCACGTCCTC   180
AAAGAATTGT GAGAGCAAAC GCGCTCCCAT TGACCTCCAC ACTCAGCCGC CAAAACAAAC   240
GTTCGAACAT TCGTGTGTTG TGCTCCTTTT CCGTTATCTT GCAGTCATCT TTTGTCGTTT   300
TTTTCTTTGT TCTTTTTGTT GAACGTGTTG CTAAGCAATT ATTACATCAA TTGAAGAAAA   360
GGCTCGCCGA TTTATTGTTG CCAGAAAGAT TCTGAGATTC TCGAAGTCGA TTTTATAATA   420
TTTAACCTTG GTTTTTGCAT TGTTTCGTTT AAAAAAACCA CTGTTTATGT GAAAAACGAT   480
TAGTTTACTA ATAAAACTAC TTTTAAACCT TTACCTTTAC CTCACCGCTC CGTGTTCATG   540
GCTCATAGAT TTTCGATACT CAAATCCAAA AATAAATTTA CGAGGGCAAT TAATGTGAAA   600
CAAAAACAAT CCTAAGATTT CCACATGTTT GACCTCTCCG GCACCTTCTT CCTTAGCCCC   660
ACCACTCCAT CACCTCTTTG GCGGTGTTCT TCGAAACCCA CTTAGGAAAG CAGTGTGTAT   720
CTCATTTGGT ATGCTCTTTT CGATTTTATA GCTCTTTGTC GCAATTTCAA TGCTTTAAAC   780
AATCCAAATC GCATTATATT TGTGCATGGA GGCAAATGAC GGGGTTGGAA TCTTAGATGA   840
GATCAGGAGC TTTCAGGGTA AACGCCCGGT TCATTTTGTA CCACATTTCA TCATTTTCCT   900
GTCGTCCTTG GTATCCTCAA CTTGTCCCGG TTTTGTTTTC GGTACACTCT TCCGTGATGC   960
CACCTGTCTC CGTCTCAATT ATCGTTTAGA AATGTGAACT GTCCAGATGG GTGACTCATA  1020
TTGCTGCTGC TACAATCCAC TTTCTTTTCT CATCGGCAGT CTTACGAGCC CATCATAAAC  1080
TTTTTTTTCC GCGAAATTTG CAATAAACCG GCCAAAAACT TTCTCCAAAT TGTTACGCAA  1140
TATATACAAT CCATAAGAAT ATCTTCTCAA TGTTTATGAT TTCTTCGCAG CACTTTCTCT  1200
TCGTGTGCTA ACATCTTATT TTTATAATAT TTCCGCTAAA ATTCCGATTT TTGAGTATTA  1260
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TGATAACCCG TAAATCGTCA CAACGCTACA GTAGTCATTT AAAGGATTAC TGTAGTTCTA  1560
GCTACGAGAT ATTTTGCGCG CCAAATATGA CTGTAATACG CATTCTCTGA ATTTTGTGTT  1620
TCCGTAATAA TTTCACAAGA TTTTGGCATT CCACTTTAAA GGCGCACAGG ATTTATTCCA  1680
ATGGGTCTCG GCACGCAAAA AGTTTGATAG ACTTTTAAAT TCTCCTTGCA TTTTTAATTC  1740
AATTACTAAA ATTTTCGTGA ATTTTTCTGT TAAAATTTTT AAAATCAGTT TTCTAATATT  1800
TTCCAGGCTG ACAAACAGAA ACAAAAACAC AACAAACATT TTAAAAATCA GTTTTCAAAT  1860
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TAAAAATAAC GATTTCTCAT TGAAAATTGT GTTTTATGTT TGCGAAAATA AAAGAGAACT    1920
GATTCAAAAC AATTTTAACA AAAAAAAACC CCAAAATTCG CCAGAAATCA AGATAAAAAA    1980
TTCAAGAGGG TCAAAATTTT CCGATTTTAC TGACTTTCAC CTTTTTTTTC GTAGTTCAGT    2040
GCAGTTGTTG GAGTTTTTGA CGAAAACTAG GAAAAAAATC GATAAAAATT ACTCAAATCG    2100
AGCTGAATTT TGAGGACAAT GTTTAAAAAA AAACACTATT TTTCCAATAA TTTCACTCAT    2160
TTTCAGACTA AATCGAAAAT CAAATCGTAC TCTGACTACG GGTCAGTAGA GAGGTCAACC    2220
ATCAGCCGAA GATGATGCGT CAAGATAGAA GGAGCTTGCT AGAGAGGAAC ATTATGATGT    2280
TCTCTAGTCA TCTAAAAGTC GATGAAATTY TCGAAGTTCT CATCGCAAAA CAAGTGTTGA    2340
ATAGTGATAA TGGAGATATG ATTAATGTGA GTTTTTAATC GAATAATAAT TTTAAAAAAA    2400
AATTGATAAT ATAAAGAATA TTTTTGCAGT CATGTGGAAC GGTTCGCGAG AAGAGACGGG    2460
AGATCGTGAA AGCAGTGCAA CGACGGRGAG ATGTGGCGTT CGACGCGTTT TATGATGCTC    2520
TTCGCTCTAC GGGACACGAA GGACTTGCTG AAGTTCTTGA ACCTCTCGCC AGATCGTAGG    2580
TTTTTAAAGT TCGGCGCAAA AGCAAGGGTC TCACGGAAAA AAGAGGCGGA TCGTAATTTT    2640
GCAACCCACC GGCACGGTTT TTTCCTCCGA AAATCGGAAA TTATGCACTT TCCCAAATAT    2700
TTGAAGTGAA ATATATTTTA TTTACTGAAA GCTCGAGTGA TTATTTATTT TTTAACACTA    2760
ATTTTCGTGG CGCAAAAGGC CATTTTGTAG ATTTGCCGAA AATACTTGTC ACACACACAC    2820
ACACACATCT CCTTCAAATA TCCCTTTTTC CAGTGTTGAC TCGAATGCTG TCGAATTCGA    2880
GTGTCCAATG TCACCGGCAA GCCATCGTCG GAGCCGCGCA TTGAGCCCCG CCGGCTACAC    2940
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GGATATCTAC TCAAGAGCAA GATCTCGTTC TCGATCGCGT GCACTTCATT CATCGGATCG    3060
ACACAATTAT TCATCTCCTC CAGTCAACGC ATTTCCCAGC CAACCTTGTA TGTTGATGCG    3120
AACACTAAAT TCTGAGAATG CGCATTACTC AACATATTTG ACGCGCAAAT ATCTCGTAGC    3180
GAAAAATACA GTAACCCTTT AAATGACTAT TGTAGTGTCG ATTTACGGGC TCGATTTTCG    3240
AAACGAATAT ATGCTCGAAT TGTGACAACG AATTTAATT TGTCATTTTT GTGTTTCTT    3300
TTGATATTTT TGATCAATTA ATAAATTATT TCCGTAAACA GACACCAGCG CTACAGTACT    3360
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TGAAAAAAAA TCATCTAACA TGTGCCAAAA CGCTTTTTTC AAGTTTCGCA GATTTTTTGA    3480
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TCATGTTGTG CAGAAAAATA GTAAAAAAGC GCATGCATTT TTCGACATTT TTTACATCGA    3720
ACGACAGCTC ACTTCACATG CTGAAGACGA GAGACGCGGA GAAATACCAC ACATCTTTCT    3780
GCGTCTCTCG TCTTCAGCAT GTGAAATGGG ATCTCGGTCG ATGTAAAAAA ATGTCGAATA    3840
ATGTAAAAAA TGCATGCGTT TTTTTACACT TTTCTGCACA AATGAATAGG GGGAAAATGT    3900
ATTAAAATAC ATTTTTTGTA TTTTTCAACA TCACATGATT AACCCCATTA TTTTTTTCGTT    3960
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GCGAAACACC TGAAAAAAAT CAAAAATTCT GCGAAAATTG AAAAAATGCA TTAAAATACA    4140
TTTTTGCATT TTTCTACATC ACATGAATGT AGAAAATTAA AAGGGAAATC AAAATTCTA    4200
GAGGATATAA TTGAATGAAA CATTGCGAAA TTAAAATGTG CGAAACGTCA AAAAGAGGA    4260
AATTTGGGTA TCAAAATCGA TCCTAAAACC AACACATTTC AGCATCCGCC AACTCTTCAT    4320
TCACCGGATG CTCTTCTCTC GGATACAGTT CAAGTCGTAA TCGCTCATTC AGCAAAGCTT    4380
CTGGACCAAC TCAATACATA TTCCATGAAG AGGATATGAA CTTTGTCGAT GCACCAACCA    4440
TAAGCCGTGT TTTCGACGAG AAAACCATGT ACAGAAACTT CTCGAGTCCT CGTGGAATGT    4500
GCCTCATCAT AAATAATGAA CACTTTGAGC AGATGCCAAC ACGGAATGGT ACCAAGGCCG    4560
ACAAGGACAA TCTTACCAAT TTGTTCAGAT GCATGGGCTA TACGGTTATT TGCAAGGACA    4620
ATCTGACGGG AAGGGTACGG CGAAATTATA TTACCCAAAC GCGAAATTTG CCATTTTGCG    4680
CCGAAAATGT GGCGCCCGGT CTCGACACGA CAATTGTGT TAAATGCAAA AATGTATAAT    4740
TTTGCAAAAA ACAAAATTTT GAACTTCCGC GAAAATGATT TACCTAGTTT CGAAATTTTC    4800
GTTTTTTCCG GCTACATTAT GTGTTTTTTC TTAGTTTTTC TATAATATTT GATGTAAAAA    4860
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          GGTGTTTCAA TATGAAATGT ATTTTTAAAA ACTTTAAAAA CCACTCCGGA AAAGCAATAA    5040
          AAATCAAAAC AACGTCACAA TTCAAATTCA AAAGTTATTC ATCCGATTTG TTTATTTTTG    5100
          CAAAATTTGA AAAAATCATG AAGGATTTAG AAAAGTTTTA TAACATTTTT TCTAGATTTT    5160
   5      TCAAAATTTT TTTTAACAAA TCGAGAAAAA GAGAATGAAA AATCGATTTT AAAAATATCC    5220
          ACAGCTTCGA GAGTTTGAAA TTACAGTACT CCTTAAAGGC GCACACCCCA TTTGCATTGG    5280
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          TGGACAATAA ACCTTCCTAA TCACCAAAAA GTAAAATTGA AATCTTCGAA AAGCCAAAAA    5400
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          TTATTGGAGT TGATGATATA CCGATTAGTA CACACGAGAT ATATGATCTT CTCAACGCGG    5700
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          GTGACAATGG ATTCCCAGTC TTGGATTCTG TCGACGGAGT TCCTGCATTT CTTCGTCGTG    5880
          GATGGGACAA TCGAGACGGG CCATTGTTCA ATTTTCTTGG ATGTGTGCGG CCGCAAGTTY    5940
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          ATTCCAGAAA GTCCCGATCG AAAAATTGCG ATATAATTAC GAAATTTGTG ATAAAATGAC    6060
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          GTGAATTGCT GATTGGTCGC AGTTTTCAGT TTAGAGGGAA TTTAAAAATC GCCTTTTCGA    6180
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          GGAGCGAAAG CCCCGTCCTG TAAACATTTT TAAATGATAA TTAATAAATT TTTGCARCAA    6300
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          ACACGGTTGG CGCGCGGCAA GTTTGCAAAA CGACGCTCCG CCTCTTTTTC TGTGCGGCTT    6960
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          ACTCGTGATT CATTGCCCAA TTGATAATTG TCTGTATCTT CTCCCCCAGT TCTCTTTCGC    7140
          CCAATTAGTT TAAAACCATG TGTATATTGT TATCCTATAC TCATTTCACT TTATCATTCT    7200
          ATCATTTCTC TTCCCATTTT CACACATTTC CATTTCTCTA CGATAATCTA AAATTATGAC    7260
  40      GTTTGTGTCT CGAACGCATA ATAATTTTAA TAACTCGTTT TGAATTTGAT TAGTTGTTGT    7320
          GCCCAGTATA TATGTATGTA CTATGCTTCT ATCAACAAAA TAGTTTCATA GATCATCACC    7380
          CCAACCCCAC CAACCTACCG TACCATATTC ATTTTTGCCG GGAATCAATT TCGATTAATT    7440
          TTAACCTATT TTTTCGCCAC AAAAAATCTA ATATTTGAAT TAACGAATAG CATTCCCATC    7500
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  45      AAATTTGTAG GTCCCCCCCA TCATTCCCG CCCATCATCT CAAATTGCAT TCTTTTTTCG    7620
          CCGTGATATC CCGATTCTGG TCAGCAAAGA TCT                                  7653
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          (2) INFORMATION FOR SEQ ID NO:2:

          (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 503 amino acids

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(B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein
       (ix) FEATURE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

       Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
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       Phe Ser Ser His Leu Lys Val Asp Glu Ile Xaa Glu Val Leu Ile Ala
                       20   25   30
       Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
                       35   40   45
       Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
               50   55   60
       Xaa Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly
       65   70   75   80
       His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp
                           85   90   95
       Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg
                       100   105   110
       Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val
                       115   120   125
       His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp
                   130   135   140
       Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser
       145   150   155   160
       Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser
                       165   170   175
       Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly
                       180   185   190
       Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr
                   195   200   205
       Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr
                   210   215   220
       Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser
       225   230   235   240
       Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met
                       245   250   255
       Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu
                   260   265   270
       Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly
                   275   280   •   285
       Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His
                   290   295   300
       Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val
       305   310   315   320
       Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp
                       325   330   335

                                 - 103 -

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     Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile
             340                 345             350
     Val Phe Val Gln Ala Cys Arg Xaa Glu Arg Arg Asp Asn Gly Phe Pro
             355                 360             365
     Val Leu Asp Ser Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp
         370             375             380
     Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro
     385             390             395                     400
     Gln Val Xaa Gln Val Trp Arg Lys Lys Pro Ser Xaa Ala Asp Ile Leu
                 405             410             415
     Ile Arg Tyr Ala Thr Thr Ala Gln Tyr Val Ser Xaa Arg Asn Ser Ala
                 420             425             430
     Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His
                 435             440             445
     Xaa Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys
                 450             455             460
     Val Xaa Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln
     465             470             475                     480
     Met Pro Xaa Met Thr Xaa Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro
                 485             490             495
     Glu Ala Arg Asn Ser Ala Val
             500
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         (2) INFORMATION FOR SEQ ID NO:3:

         (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1373 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: cDNA
         (ix) FEATURE:

            (A) NAME/KEY: Coding Sequence
            (B) LOCATION: 18...1229
            (D) OTHER INFORMATION: /product= "human interleukin-1 beta
     convertase"

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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                        Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys
                         1           5           •           10

     CTG TTT ATC CGT TCC ATG GGT GAA GGT ACA ATA AAT GGC TTA CTG GAT     98
     Leu Phe Ile Arg Ser Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp
             15              20              25

     GAA TTA TTA CAG ACA AGG GTG CTG AAC AAG GAA GAG ATG GAG AAA GTA    146
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                    Glu Leu Leu Gln Thr Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val
                                    30                  35                  40

      5     AAA CGT GAA AAT GCT ACA GTT ATG GAT AAG ACC CGA GCT TTG ATT GAC     194
            Lys Arg Glu Asn Ala Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp
                    45                  50                  55

            TCC GTT ATT CCG AAA GGG GCA CAG GCA TGC CAA ATT TGC ATC ACA TAC     242
            Ser Val Ile Pro Lys Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr
            60                  65                  70                  75

     10     ATT TGT GAA GAA GAC AGT TAC CTG GCA GGG ACG CTG GGA CTC TCA GCA     290
            Ile Cys Glu Glu Asp Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala
                            80                  85                  90

            GAT CAA ACA TCT GGA AAT TAC CTT AAT ATG CAA GAC TCT CAA GGA GTA     338
            Asp Gln Thr Ser Gly Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val
                            95                  100                 105

     15     CTT TCT TCC TTT CCA GCT CCT CAG GCA GTG CAG GAC AAC CCA GCT ATG     386
            Leu Ser Ser Phe Pro Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met
                        110                 115                 120

            CCC ACA TCC TCA GGC TCA GAA GGG AAT GTC AAG CTT TGC TCC CTA GAA     434
            Pro Thr Ser Ser Gly Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu
     20                 125                 130                 135

            GAA GCT CAA AGG ATA TGG AAA CAA AAG TCG GCA GAG ATT TAT CCA ATA     482
            Glu Ala Gln Arg Ile Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile
            140                 145                 150                 155

            ATG GAC AAG TCA AGC CGC ACA CGT CTT GCT CTC ATT ATC TGC AAT GAA     530
     25     Met Asp Lys Ser Ser Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu
                            160                 165                 170

            GAA TTT GAC AGT ATT CCT AGA AGA ACT GGA GCT GAG GTT GAC ATC ACA     578
            Glu Phe Asp Ser Ile Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr
                            175                 180                 185

     30     GGC ATG ACA ATG CTG CTA CAA AAT CTG GGG TAC AGC GTA GAT GTG AAA     626
            Gly Met Thr Met Leu Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys
                        190                 195                 200

            AAA AAT CTC ACT GCT TCG GAC ATG ACT ACA GAG CTG GAG GCA TTT GCA     674
            Lys Asn Leu Thr Ala Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala
     35                 205                 210                 215

            CAC CGC CCA GAG CAC AAG ACC TCT GAC AGC ACG TTC CTG GTG TTC ATG     722
            His Arg Pro Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met
            220                 225                 230                 235
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    TCT CAT GGT ATT CGG GAA GGC ATT TGT GGG AAG AAA CAC TCT GAG CAA      770
    Ser His Gly Ile Arg Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln
                240                 245             250

    GTC CCA GAT ATA CTA CAA CTC AAT GCA ATC TTT AAC ATG TTG AAT ACC      818
 5  Val Pro Asp Ile Leu Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr
                255                 260             265

    AAG AAC TGC CCA AGT TTG AAG GAC AAA CCG AAG GTG ATC ATC ATC CAG      866
    Lys Asn Cys Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln
                270                 275             280

10  GCC TGC CGT GGT GAC AGC CCT GGT GTG GTG TGG TTT AAA GAT TCA GTA      914
    Ala Cys Arg Gly Asp Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val
                285                 290             295

    GGA GTT TCT GGA AAC CTA TCT TTA CCA ACT ACA GAA GAG TTT GAG GAT      962
    Gly Val Ser Gly Asn Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp
15  300                 305             310                 315

    GAT GCT ATT AAG AAA GCC CAC ATA GAG AAG GAT TTT ATC GCT TTC TGC     1010
    Asp Ala Ile Lys Lys Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys
                320                 325             330

    TCT TCC ACA CCA GAT AAT GTT TCT TGG AGA CAT CCC ACA ATG GGC TCT     1058
20  Ser Ser Thr Pro Asp Asn Val Ser Trp Arg His Pro Thr Met Gly Ser
                335                 340             345

    GTT TTT ATT GGA AGA CTC ATT GAA CAT ATG CAA GAA TAT GCC TGT TCC     1106
    Val Phe Ile Gly Arg Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser
                350                 355             360

25  TGT GAT GTG GAG GAA ATT TTC CGC AAG GTT CGA TTT TCA TTT GAG CAG     1154
    Cys Asp Val Glu Glu Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln
                365                 370             375

    CCA GAT GGT AGA GCG CAG ATG CCC ACC ACT GAA AGA GTG ACT TTG ACA     1202
    Pro Asp Gly Arg Ala Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr
30  380                 385             390                 395

    AGA TGT TTC TAC CTC TTC CCA GGA CAT TAAAATAAGG AAACTGTATG AATGTCT    1256
    Arg Cys Phe Tyr Leu Phe Pro Gly His
                400

    GCGGGCAGGA AGTGAAGAGA TCGTTCTGTA AAAGGTTTTT GGAATTATGT CTGCTGAATA   1316
35  ATAAACTTTT TTTGAAATAA TAAATCTGGT AGAAAAATGA AAAAAAAAAA AAAAAA        1373
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 amino acids

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(B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (ix) FEATURE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
 1   5   10   15
Met Gly Glu Gly Thr Ile Asn Gly Leu Xaa Asp Glu Leu Leu Gln Thr
            20   25   30
Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
        35   40   45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
        50   55   60
Xaa Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
65   70   75   80
Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
                85   90   95
Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
            100   105   110
Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
        115   120   125
Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile
        130   135   140
Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
145   150   155   160
Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
                165   170   175
Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
            180   185   190
Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
            195   200   205
Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
        210   215   220
Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
225   230   235   240
Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
            245   250   255
Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
            260   265   270
Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Xaa Arg Xaa Asp
        275   280   ·   285
Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
        290   295   300
Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
305   310   315   320
Ala His Ile Xaa Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
            325   330   335

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```
Asn Val Ser Xaa Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
            340                 345                 350
Leu Ile Glu His Met Gln Glu Tyr Xaa Cys Ser Cys Asp Val Glu Glu
            355                 360                 365
Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
            370                 375                 380
Gln Met Pro Thr Thr Xaa Arg Val Xaa Leu Thr Arg Cys Phe Tyr Leu
385                 390                 395                 400
Phe Pro Gly His
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 505 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Met Arg Gln Asp Arg Trp Leu Leu Glu Arg Asn Ile Leu Glu Phe
1               5                   10                  15
Ser Ser Lys Leu Gln Ala Asp Leu Ile Leu Asp Val Leu Ile Ala Lys
            20                  25                  30
Gln Val Leu Asn Ser Asp Asn Gly Asp Val Ile Asn Ser Cys Arg Thr
            35                  40                  45
Glu Arg Asp Asn Glu Lys Glu Ile Val Lys Ala Val Gln Arg Arg Gly
        50                  55                  60
Asp Glu Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Asp Thr Gly His
65              70                  75                  80
Asn Asp Leu Ala Asp Val Leu Met Pro Leu Ser Arg Pro Xaa Xaa Xaa
                85                  90                  95
Asn Pro Val Pro Met Glu Cys Pro Met Ser Pro Ser Ser His Arg Arg
            100                 105                 110
Ser Arg Ala Leu Ser Pro Pro Xaa Tyr Ala Ser Pro Thr Arg Val His
            115                 120                 125
Arg Asp Ser Ile Ser Ser Val Ser Ser Phe Thr Ser Thr Tyr Gln Asp
            130                 135                 140
Val Tyr Ser Arg Ala Arg Ser Ser Ser Arg Ser Ser Arg Pro Leu Gln
145                 150                 155                 160
Ser Ser Asp Arg His Asn Tyr Met Ser Ala Ala Thr Ser Phe Pro Ser
                165                 170                 175
Gln Pro Xaa Ser Ala Asn Ser Ser Phe Thr Gly Cys Ala Ser Leu Gly
            180                 185                 190
Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Thr Ser Ala Gln Ser
            195                 200                 205
Gln Tyr Ile Phe His Glu Glu Asp Met Asn Tyr Val Asp Ala Pro Thr
            210                 215                 220
```

```
Ile His Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser
225             230             235             240
Pro Arg Gly Leu Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met
            245             250             255
Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Ile
        260             265             270
Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly
        275             280             285
Arg Glu Met Leu Ser Thr Ile Arg Ser Phe Gly Arg Asn Asp Met His
    290             295             300
Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Xaa Asn Val
305             310             315             320
Ile Ile Gly Val Asp Asp Val Ser Val Asn Val His Glu Ile Tyr Asp
            325             330             335
Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Leu
            340             345             350
Val Phe Val Gln Ala Cys Arg Gly Glu Arg Arg Asp Asn Gly Phe Pro
            355             360             365
Val Leu Asp Ser Val Asp Gly Val Pro Ser Leu Ile Arg Arg Gly Trp
370             375             380
Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro
385             390             395             400
Gln Val Gln Gln Val Trp Arg Lys Lys Pro Ser Gln Ala Asp Met Leu
            405             410             415
Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val Ser Trp Arg Asn Ser Ala
            420             425             430
Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Leu His
            435             440             445
Ala Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys
450             455             460
Val Ala Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln
465             470             475             480
Met Pro Glu Leu Thr Ser Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro
            485             490             495
Glu Asp Arg Gly Arg Asn Ser Ala Val
        500             505
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 479 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Thr Val Ser Leu Ser Leu Ile Ile Ala Arg Gln Val Leu Asn Ser Asp
  1             5             10             15
```

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```
    Asn Gly Asp Met Ile Asn Ser Cys Arg Thr Glu Arg Asp Asn Glu Lys
             20              25              30
    Glu Ile Val Lys Ala Val Gln Arg Arg Gly Asp Glu Ala Phe Asp Ala
             35              40              45
  5 Phe Tyr Asp Ala Leu Arg Asp Thr Gly His Asn Asp Leu Ala Asp Val
             50              55              60
    Leu Met Pro Leu Ser Arg Pro Val Asp Ser Asn Pro Val Pro Met Glu
    65              70              75              80
    Cys Pro Met Ser Pro Ser Ser His Arg Arg Ser Arg Ala Leu Ser Pro
 10              85              90              95
    Pro Xaa Tyr Ala Ser Pro Thr Arg Val His Arg Asp Ser Ile Ser Ser
            100             105             110
    Val Ser Ser Phe Thr Ser Thr Tyr Gln Asp Val Tyr Ser Arg Ala Thr
            115             120             125
 15 Ser Ser Ser Pro Leu Gln Thr Ser Asp Arg His Asn Tyr Val Ser Ala
            130             135             140
    Ser Thr Ser Phe Gln Ser Gln Pro Ala Ser Ala Asn Ser Ser Phe Thr
    145             150             155             160
    Gly Ser Ala Ser Leu Gly Tyr Ser Ser Ser Arg Thr Arg Ser Tyr Ser
 20             165             170             175
    Lys Thr Ser Ala His Ser Gln Tyr Ile Phe His Glu Glu Asp Met Asn
            180             185             190
    Tyr Val Asp Ala Pro Thr Ile His Arg Val Phe Asp Glu Lys Thr Met
            195             200             205
 25 Tyr Arg Asn Phe Ser Thr Pro Arg Gly Leu Cys Leu Ile Ile Asn Asn
            210             215             220
    Glu His Phe Glu Gln Met Pro Thr Arg Asn Gly Thr Lys Pro Asp Lys
    225             230             235             240
    Asp Asn Ile Ser Asn Ile Phe Arg Cys Met Gly Tyr Ile Val His Cys
 30             245             250             255
    Lys Asp Asn Leu Thr Gly Arg Glu Met Met Ser Thr Ile Arg Ser Phe
            260             265             270
    Gly Arg Asn Asp Thr His Gly Asp Ser Ala Ile Leu Val Ile Leu Ser
            275             280             285
 35 His Gly Glu Xaa Asn Val Ile Ile Gly Val Asp Asp Val Ser Val Asn
            290             295             300
    Val His Glu Ile Tyr Xaa Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu
    305             310             315             320
    Ala Asn Lys Pro Lys Leu Val Phe Val Gln Ala Cys Arg Gly Glu Arg
 40             325             330             335
    Arg Asp Val Gly Phe Pro Val Leu Asp Ser Val Asp Gly Val Pro Ser
            340             345             350
    Leu Ile Arg Arg Gly Trp Asp Lys Gly Asp Gly Pro Leu Phe Asn Phe
            355             360             365
 45 Leu Gly Cys Val Arg Pro Gln Ala Gln Gln Val Trp Arg Lys Lys Pro
            370             375             380
    Ser Gln Ala Asp Met Leu Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val
    385             390             395             400
    Ser Trp Arg Asn Ser Ala Arg Gly Ser Trp Phe Ile Gln Ala Val Cys
 50             405             410             415
    Glu Val Phe Ser Leu His Ala Lys Asp Met Asp Val Val Glu Leu Leu
```

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```
                    420                  425                   430
    Thr Glu Val Asn Lys Lys Val Ala Cys Gly Phe Gln Thr Ser Gln Gly
            435                  440                   445
    Ala Asn Ile Leu Lys Gln Met Pro Glu Leu Thr Ser Arg Leu Leu Lys
            450                  455                   460
    Lys Phe Tyr Phe Trp Pro Glu Asp Arg Asn Arg Ser Ser Ala Val
    465                  470                   475
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCATCGACTT TTAGATGACT AGAGAACATC   30

    (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGCACTGC TTTCACGATC TCCCGTCTCT   30

    (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTTAATTAC CCAAGTTTGA G   21

    (2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5   GGTTTTAACC AGTTACTCAA G   21

            (2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 19 base pairs
          (B) TYPE: nucleic acid
10   (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

        CCGGTGACAT TGGACACTC   19

            (2) INFORMATION FOR SEQ ID NO:12:

15   (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

        ACTATTCAAC ACTTG   15

            (2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 171 amino acids
25   (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein
        (ix) FEATURE:
30   (D) OTHER INFORMATION: Xaa at position 117 is Ala or Val.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

        Met Leu Thr Val Gln Val Tyr Arg Thr Ser Gln Lys Cys Ser Ser Ser
         1   5   10   15

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```
        Lys His Val Val Glu Val Leu Leu Asp Pro Leu Gly Thr Ser Phe Cys
                    20              25              30
        Ser Leu Leu Pro Pro Pro Leu Leu Leu Tyr Glu Thr Asp Arg Gly Val
                    35              40              45
    5   Asp Gln Gln Asp Gly Lys Asn His Thr Gln Ser Pro Gly Cys Glu Glu
                    50              55              60
        Ser Asp Ala Gly Lys Glu Glu Leu Met Lys Met Arg Leu Pro Thr Arg
        65              70              75              80
        Ser Asp Met Ile Cys Gly Tyr Ala Cys Leu Lys Gly Asn Ala Ala Met
   10                   85              90              95
        Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile Glu Ala Leu Thr Gln Val
                    100             105             110
        Phe Ser Glu Arg Xaa Cys Asp Met His Val Ala Asp Met Leu Val Lys
                    115             120             125
   15   Val Asn Ala Leu Ile Lys Glu Arg Glu Gly Tyr Ala Pro Gly Thr Glu
                    130             135             140
        Phe His Arg Cys Lys Glu Met Ser Glu Tyr Cys Ser Thr Leu Cys Gln
        145             150             155             160
        Gln Leu Tyr Leu Phe Pro Gly Tyr Pro Pro Thr
   20                   165             170


            (2)  INFORMATION FOR SEQ ID NO:14:


            (i)  SEQUENCE CHARACTERISTICS:
                 (A)  LENGTH: 402 amino acids
                 (B)  TYPE: amino acid
   25            (C)  STRANDEDNESS: single
                 (D)  TOPOLOGY: linear


            (ii) MOLECULE TYPE: protein


            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:


        Met Ala Asp Lys Ile Leu Arg Ala Lys Arg Lys Gln Phe Ile Asn Ser
   30    1               5               10              15
        Val Ser Ile Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Lys
                    20              25              30
        Arg Val Leu Asn Gln Glu Glu Met Asp Lys Ile Lys Leu Ala Asn Ile
                    35              40              45
   35   Thr Ala Met Asp Lys Ala Arg Asp Leu Cys Asp His Val Ser Lys Lys
                    50              55              60
        Gly Pro Gln Ala Ser Gln Ile Phe Ile Thr Tyr Ile Cys Asn Glu Asp
        65              70              75              80
        Cys Tyr Leu Ala Gly Ile Leu Glu Leu Gln Ser Ala Pro Ser Ala Glu
   40                   85              90              95
        Thr Phe Val Ala Thr Glu Asp Ser Lys Gly Gly His Pro Ser Ser Ser
                    100             105             110
        Glu Thr Lys Glu Glu Gln Asn Lys Glu Asp Gly Thr Phe Pro Gly Leu
                    115             120             125
   45   Thr Gly Thr Leu Lys Phe Cys Pro Leu Glu Lys Ala Gln Lys Leu Trp
                    130             135             140
```

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```
    Lys Glu Asn Pro Ser Glu Ile Tyr Pro Ile Met Asn Thr Thr Thr Arg
    145             150             155             160
    Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr Glu Phe Gln His Leu Ser
                165             170             175
 5  Pro Arg Val Gly Ala Gln Val Asp Leu Arg Glu Met Lys Leu Leu Leu
                180             185             190
    Glu Asp Leu Gly Tyr Thr Val Lys Val Lys Glu Asn Leu Thr Ala Leu
                195             200             205
    Glu Met Val Lys Glu Val Lys Glu Phe Ala Ala Cys Pro Glu His Lys
10  210             215             220
    Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Gln Glu
    225             230             235             240
    Gly Ile Cys Gly Thr Thr Tyr Ser Asn Glu Val Ser Asp Ile Leu Lys
                245             250             255
15  Val Asp Thr Ile Phe Gln Met Met Asn Thr Leu Lys Cys Pro Ser Leu
                260             265             270
    Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Glu Lys
                275             280             285
    Gln Gly Val Val Leu Leu Lys Asp Ser Val Arg Asp Ser Glu Glu Asp
20  290             295             300
    Phe Leu Thr Asp Ala Ile Phe Glu Asp Asp Gly Ile Lys Lys Ala His
    305             310             315             320
    Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp Asn Val
                325             330             335
25  Ser Trp Arg His Pro Val Arg Gly Ser Leu Phe Ile Glu Ser Leu Ile
                340             345             350
    Lys His Met Lys Glu Tyr Ala Trp Ser Cys Asp Leu Glu Asp Ile Phe
                355             360             365
    Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Glu Phe Arg Leu Gln Met
30  370             375             380
    Pro Thr Ala Asp Arg Val Thr Leu Thr Lys Arg Phe Tyr Leu Phe Pro
    385             390             395             400
    Gly His
```

1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 4 amino acids
5   (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
10   (D) OTHER INFORMATION: Peptide has an acetyl group at the
amino terminus and an aldehyde group at the carboxyl terminus.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Val Ala Asp
1

15   (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 4 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Val Ala Asp
1

25   (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 4 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
        (D) OTHER INFORMATION: Xaa at position 2 is D-Ala. Peptide
has an acetyl group at the amino terminus and an aldehyde group at
35 the carboxyl terminus.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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```
Tyr Xaa Ala Asp
 1
```

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 4 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
       (D) OTHER INFORMATION: Peptide has an acetyl group at the
amino terminus and an aldehyde group at the carboxyl terminus.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Tyr Val Lys Asp
 1
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 354 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (v) FRAGMENT TYPE: C-terminal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser Ser Asp Arg His Asn
 1               5                  10                  15
Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser Gln Pro Ser Ser Ala
            20                  25                  30
Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly Tyr Ser Ser Ser Arg
            35                  40                  45
Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr Gln Tyr Ile Phe His
        50                  55                  60
Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr Ile Ser Arg Val Phe
65                  70                  75                  80
Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser Pro Arg Gly Met Cys
                85                  90                  95
Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met Pro Thr Arg Asn Gly
                100                 105                 110
Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu Phe Arg Cys Met Gly
        115                 120                 125
Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly Arg Gly Met Leu Leu
```

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```
                130                 135                 140
Thr Ile Arg Asp Phe Ala Lys His Glu Ser His Gly Asp Ser Ala Ile
145                 150                 155                 160
Leu Val Ile Leu Ser His Gly Glu Glu Asn Val Ile Ile Gly Val Asp
                    165                 170                 175
Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp Leu Leu Asn Ala Ala
                    180                 185                 190
Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile Val Phe Val Gln Ala
                    195                 200                 205
Cys Arg Xaa Glu Arg Arg Asp Asn Gly Phe Pro Val Leu Asp Ser Val
210                 215                 220
Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp Asp Asn Arg Asp Gly
225                 230                 235                 240
Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro Gln Val Xaa Gln Val
                    245                 250                 255
Trp Arg Lys Lys Pro Ser Xaa Ala Asp Ile Leu Ile Arg Tyr Ala Thr
                260                 265                 270
Thr Ala Gln Tyr Val Ser Xaa Arg Asn Ser Ala Arg Gly Ser Trp Phe
                275                 280                 285
Ile Gln Ala Val Cys Glu Val Phe Ser Thr His Xaa Lys Asp Met Asp
                290                 295                 300
Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys Val Xaa Cys Gly Phe
305                 310                 315                 320
Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln Met Pro Xaa Met Thr
                    325                 330                 335
Xaa Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro Glu Ala Arg Asn Ser
                340                 345                 350
Ala Val
```

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 131 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (v) FRAGMENT TYPE: C-terminal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp Asp Asn Arg Asp
1                   5                   10                  15
Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro Gln Val Xaa Gln
                    20                  25                  30
Val Trp Arg Lys Lys Pro Ser Xaa Ala Asp Ile Leu Ile Arg Tyr Ala
                35                  40                  45
Thr Thr Ala Gln Tyr Val Ser Xaa Arg Asn Ser Ala Arg Gly Ser Trp
                50                  55                  60
```

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```
Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His Xaa Lys Asp Met
65                  70                  75                  80
Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys Val Xaa Cys Gly
                85                  90                  95
Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln Met Pro Xaa Met
            100                 105                 110
Thr Xaa Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro Glu Ala Arg Asn
        115                 120                 125
Ser Ala Val
        130
```

```
        (2)  INFORMATION FOR SEQ ID NO:22:

            (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH: 223 amino acids
                (B)  TYPE: amino acid
                (C)  STRANDEDNESS: single
                (D)  TOPOLOGY: linear

            (ii)  MOLECULE TYPE: protein
            (v)  FRAGMENT TYPE: internal

            (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser Ser Asp Arg His Asn
    1           5                   10                  15
Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser Gln Pro Ser Ser Ala
            20                  25                  30
Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly Tyr Ser Ser Ser Arg
            35                  40                  45
Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr Gln Tyr Ile Phe His
        50                  55                  60
Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr Ile Ser Arg Val Phe
65                  70                  75                  80
Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser Pro Arg Gly Met Cys
                85                  90                  95
Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met Pro Thr Arg Asn Gly
            100                 105                 110
Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu Phe Arg Cys Met Gly
        115                 120                 125
Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly Arg Gly Met Leu Leu
    130                 135                 140
Thr Ile Arg Asp Phe Ala Lys His Glu Ser His Gly Asp Ser Ala Ile
145                 150                 155                 160
Leu Val Ile Leu Ser His Gly Glu Glu Asn Val Ile Ile Gly Val Asp
                165                 170                 175
Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp Leu Leu Asn Ala Ala
            180                 185                 190
Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile Val Phe Val Gln Ala
        195                 200                 205
Cys Arg Xaa Glu Arg Arg Asp Asn Gly Phe Pro Val Leu Asp Ser
```

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 294 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Phe Pro Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser
 1               5                  10              15
Ser Gly Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln
            20                  25                  30
Arg Ile Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys
            35                  40                  45
Ser Ser Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp
        50                  55                  60
Ser Ile Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr
65                  70                  75                  80
Met Leu Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu
                85                  90                  95
Thr Ala Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro
            100                 105                 110
Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly
            115                 120                 125
Ile Arg Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp
        130                 135                 140
Ile Leu Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys
145                 150                 155                 160
Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Xaa Arg
                165                 170                 175
Xaa Asp Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser
            180                 185                 190
Gly Asn Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile
            195                 200                 205
Lys Lys Ala His Ile Xaa Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr
            210                 215                 220
Pro Asp Asn Val Ser Xaa Arg His Pro Thr Met Gly Ser Val Phe Ile
225                 230                 235                 240
Gly Arg Leu Ile Glu His Met Gln Glu Tyr Xaa Cys Ser Cys Asp Val
                245                 250                 255
Glu Glu Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly
            260                 265                 270
Arg Ala Gln Met Pro Thr Thr Xaa Arg Val Xaa Leu Thr Arg Cys Phe
            275                 280                 285
```

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Tyr Leu Phe Pro Gly His
290

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Ser Val Gly Val Ser Gly Asn Leu Ser Leu Pro Thr Thr Glu Glu Phe
1               5                   10                  15
Glu Asp Asp Ala Ile Lys Lys Ala His Ile Xaa Lys Asp Phe Ile Ala
                20              25              30
Phe Cys Ser Ser Thr Pro Asp Asn Val Ser Xaa Arg His Pro Thr Met
            35                  40              45
Gly Ser Val Phe Ile Gly Arg Leu Ile Glu His Met Gln Glu Tyr Xaa
        50                  55                  60
Cys Ser Cys Asp Val Glu Glu Ile Phe Arg Lys Val Arg Phe Ser Phe
65              70                  75                  80
Glu Gln Pro Asp Gly Arg Ala Gln Met Pro Thr Thr Xaa Arg Val Xaa
                85                  90                  95
Leu Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Phe Pro Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser
1               5                   10                  15
Ser Gly Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln
                20              25              30
Arg Ile Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys
                35              40              45
Ser Ser Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp
```

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```
                  50                    55                    60
      Ser Ile Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr
      65                    70                    75                    80
      Met Leu Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu
  5                         85                    90                    95
      Thr Ala Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro
                          100                   105                   110
      Glu His Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly
                          115                   120                   125
 10   Ile Arg Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp
                          130                   135                   140
      Ile Leu Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys
      145                   150                   155                   160
      Pro Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Xaa Arg
 15                       165                   170                   175
      Xaa Asp Ser Pro Gly Val Val Trp Phe Lys Asp
                          180                   185
```

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 172 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (v) FRAGMENT TYPE: internal

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
      Met Leu Thr Val Gln Val Tyr Arg Thr Ser Gln Lys Cys Ser Ser Ser
      1                   5                    10                    15
      Lys His Val Val Glu Val Leu Leu Asp Pro Leu Gly Thr Ser Phe Cys
 30                       20                    25                    30
      Ser Leu Leu Pro Pro Pro Leu Leu Leu Tyr Glu Thr Asp Arg Gly Val
                          35                    40                    45
      Asp Gln Gln Asp Gly Lys Asn His Thr Gln Ser Pro Gly Cys Glu Glu
                          50                    55                    60
 35   Ser Asp Ala Gly Lys Glu Glu Leu Met Lys Met Arg Leu Pro Thr Arg
      65                    70                    75                    80
      Ser Asp Met Ile Cys Gly Tyr Ala Cys Leu Lys Gly Asn Ala Ala Met
                          85                    90                    95
      Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile Glu Ala Leu Thr Gln Val
 40                      100                   105                   110
      Phe Ser Glu Arg Ala Xaa Cys Asp Met His Val Ala Asp Met Leu Val
                          115                   120                   125
      Lys Val Asn Ala Leu Ile Lys Glu Arg Glu Gly Tyr Ala Pro Gly Thr
                          130                   135                   140
 45   Glu Phe His Arg Cys Lys Glu Met Ser Glu Tyr Cys Ser Thr Leu Cys
```

```
      145                    150                   155                        160
      Gln Gln Leu Tyr Leu Phe Pro Gly Tyr Pro Pro Thr
                        165                   170
```

        (2) INFORMATION FOR SEQ ID NO:27:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 172 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: protein
            (v) FRAGMENT TYPE: internal

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
      Met Leu Thr Val Gln Val Tyr Arg Thr Ser Gln Lys Cys Ser Ser Ser
        1               5                   10                  15
      Lys His Val Val Glu Val Leu Leu Asp Pro Leu Gly Thr Ser Phe Cys
                        20                  25                  30
      Ser Leu Leu Pro Pro Pro Leu Leu Leu Tyr Glu Thr Asp Arg Gly Val
                    35                  40                  45
      Asp Gln Gln Asp Gly Lys Asn His Thr Gln Ser Pro Gly Cys Glu Glu
            50                  55                  60
      Ser Asp Ala Gly Lys Glu Glu Leu Met Lys Met Arg Leu Pro Thr Arg
      65                  70                  75                      80
      Ser Asp Met Ile Cys Gly Tyr Ala Cys Leu Lys Gly Asn Ala Ala Met
                        85                  90                  95
      Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile Glu Ala Leu Thr Gln Val
                    100                 105                 110
      Phe Ser Glu Arg Val Xaa Cys Asp Met His Val Ala Asp Met Leu Val
                    115                 120                 125
      Lys Val Asn Ala Leu Ile Lys Glu Arg Glu Gly Tyr Ala Pro Gly Thr
            130                 135                 140
      Glu Phe His Arg Cys Lys Glu Met Ser Glu Tyr Cys Ser Thr Leu Cys
      145                 150                 155                 160
      Gln Gln Leu Tyr Leu Phe Pro Gly Tyr Pro Pro Thr
                        165                 170
```

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